

FIGURE 1

1 AGCTCCAGCCTAGGCGTTCTACCTGGAAAGATGCAGGGGCCAGTACCTAGGACTGAGGA 60
 61 AGATGGCTGACATCCAGAACAATTCGCTGGACAGCCAGGAGCGTAGGGCTGTGGCAG 120
 121 TGCCCTGATCTTTGCCCTCAATCTTCCTGTGGGCAATGGTGGCAATGGGCTGGTGTGG 180
 181 CTGTGCTACTGCAGCCTGGCCCCAAGTGCCCTGGCAGGAGCCAAAGCAGTACCCACAGATCTCT 240
 241 TCATCCTCAACTTGGCCGTGGCCGACCTTTGGCTTCATCTGTGCTGCAAGACGGTACATC 300
 301 CAGCCATCTACACACTGGATGCCCTGGCTCTTTGGGCTTTTCGGGCTTCACCCCTGCCGCTCCCTGGACA 360
 361 TGCTCATCTACCTACCATGTATGCCAGCAGCTTCACCCCTGGCGCACCCCGCGCAACGCGC 420
 421 GGTACCTGGCTGTGGGACCCACTGCGCTCCAGAGCCCTGCGCACCCCGCGCTACCTAAGCT 480
 481 GCGCCGCGTGGGCTCGTGTGGCTGCTGGCGGCTCTCTTTCCGCGCCCTACCTAAGCT 540
 541 ATTACGGCACGGTGGCTACGGCGGCTCGAGCTCTGCTGCGTGGCGGCTACCTGCTGCGGCTGG 600
 601 GCGGCGCGCTGGACGTGGCCACCTTCGCGCGGCTACCTGCTGCGGCTGGTCCCGCGGCG 660
 661 TGAGCCTGGCTACGGACGACCGCTATGTTTCCATATGGCGCGCTGGTCCCGCGGCGAG 720
 721 CGCGGCGACAGAGCGCGCAGACGGCGACCGCGCGGCGGAGCGGCGCATGCTGCTTCTGGT 780
 781 TGGCGCGCTTACGCGCTTTGCTGGGCGCGCACCGCGCTCATCTGCTGCGCTGCGCATGCTCG 840
 841 ACGGCGCGCTTCAGCCCGGCGCACCTACGCTGCTGCGCTGCGCTGCGGCTGCGGCTTCCGCG 900
 901 CCTACGCCAACTCCTGCGCTTAACCGCTCGTCTACTGCTGCGCTGCGGCTGCGGCTGCGGCTC 960
 961 CGCGCTTCGCGCGCTGTGGCCCTGCGGCGCTCGCGCGCACCGCGCACCGCGGCTGCGGCTC 1020
 1021 ATCGAGCCCTCCGTGCTGTCAGCCCGGCTCTCGGCGCGCGCGGCTATCCCGCGGAGAG 1080
 1081 CCAGGCCCTCGTGGTGGAGTATGGAGCCAGAGGGGATGCTCTGCGTGGTGGTGGAGAGA 1140
 1141 CTAGACTAACCCCTGTCCCGGAGGACCTCAATAACCCCTGCGCGCTTGGACTCTGACGTC 1200
 1201 TGTCAAGATGCCACCAAGGAACATCTAGGGAACGGCAGTCTCGCCAGGCTCCACCAAAAA 1260
 1261 GCAGAAAGCAAAGTTGCAGGG 1280

FIGURE 2

20	V	A	F	A	L	R	R	Y	R	V	A	V	Y	A	A	H	A	T
40	A	L	L	Q	H	D	A	S	A	V	G	A	W	L	R	A	D	E
60	V	V	D	F	V	L	N	L	D	A	A	L	F	C	F	R	G	G
80	A	L	T	P	T	S	R	Y	E	V	P	M	C	H	H	H	P	G
100	G	G	T	V	K	V	P	P	W	P	G	A	L	S	R	H	Y	G
120	V	N	S	C	C	A	T	A	A	L	V	R	I	A	S	H	G	R
140	S	G	S	C	V	A	R	S	P	L	A	G	L	L	A	R	A	L
160	G	V	P	L	F	L	L	F	V	Y	A	A	A	R	L	H	P	A
180	P	M	E	I	A	T	A	L	C	G	W	R	H	C	S	R	G	D
200	S	G	Q	F	G	F	R	A	L	A	L	G	H	A	Y	R	S	G
220	D	L	W	C	F	S	S	A	E	A	F	T	P	Y	V	R	S	R
240	L	L	A	L	L	S	R	L	L	F	C	A	G	T	L	G	A	P
260	S	F	S	D	W	A	L	L	A	T	L	R	W	A	P	C	P	E
280	I	I	P	A	A	Y	P	W	G	A	T	R	C	P	N	P	Q	M
300	N	L	G	V	D	M	H	V	Y	V	R	R	L	S	L	W	V	S
320	Q	A	P	A	L	T	R	L	R	D	G	A	A	F	C	L	R	W
340	I	F	Q	L	T	L	V	G	V	L	Y	E	Y	A	S	R	R	G
360	D	I	L	N	Y	Y	A	V	T	A	A	A	L	F	N	R	L	R
370	A	V	L	L	I	I	L	A	G	R	L	A	A	R	A	F	A	P
	M	P	V	I	A	L	Y	A	Y	R	S	A	A	G	Y	R	R	R

FIGURE 3

1 CACTCAGCGATGACTTTGGCTCTGCTCTCCCCCTCCCTCCATCTCCACGAGCTTCCAGCCC 60
 61 AGAACACCTGGCCAGACCCAGGTCGGGGAGTTAGATCCCGGGGTCAAGCAACCAGAACT 120
 21 AGAACACCTGGCCAGACCCAGGTCGGGGAGTTAGATCCCGGGGTCAAGCAACCAGAACT 180
 31 GGGGCTCTTGGCTGAGGATTCAGCTTCTCTTCCAGGTGCCCTGCTGATGGGAGATG 240
 81 GCTGATGCCCAGAACATTTCACTGGACAGCCAGGAGTGTGGGGGCCGTGGCAGTGGCTT 300
 141 GTGGTCTTTGCCCTAATCTTCTCTCTGGGACAGTGGGCAATGGGCTGGTGTCTGGCAGT 360
 161 CTCTGCAGCCCTGGCCCGAGTGGCTGGCAGGAGCCTGGCAGCACCAAGGACCTGTTCATC 420
 181 CTCAACCTGGCGGTGGCTGACCTCTGCTTCACTCTGTGCTGCTGCTGCTGCTGCTGCTG 480
 201 ATCTACACGCTGGATGCCCTGGCTCTTTGGGGCCCTCGTCTGCAAGGCCCTGCACCTGCT 540
 221 ATCTACCTACCATGTACGCCAGCAGCTTTACGCTGGCTGCTGCTGCTGCTGCTGCTGCTG 600
 241 CTGGCCCTGGGCAACCCGCTGGCTCGCGGCCCTGCGACGCCGCCCTACCTCAGCTACTAC 660
 261 GCAGTGGGCTGGTGGCTGGCTGGCGGCGCTCTTCTCGGCGCCCTGGGAGGACGCCGCCGC 720
 281 GGACCCGTGGCTACGGCGGCTGGAGCTCTGCTGCGGCTACCTGCTGCCCTGGGCTGTGGT 780
 301 CGGCCCTGACGTGGCCACCTTCGCTGCCGCTACCTGCTGCCCTGGGCTGCCGCGCGCGG 840
 321 CTGGCCCTACGGCGCACGCTGGCTTCTGTGGGCGCGCTGGCTGCCGCGCGCGCTGGCC 900
 341 GCGGCCGAGCGCGCGGAGGGCGACGGGCGCGCGCGCGCTCATCTGCTGCTTCTGCTACGG 960
 361 GCGCTTACGCGCTCTGCTGGGTCCGACACCGCTGCGCTGCGCTGCGCTGCGCTGCGCTAC 1020
 381 CGCTTCGCTTACGCGCGCGCACCTACGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 1080
 401 GCCAACTCCTGCTCAACCCGCTCGTCTACGCTGCGCTGCGCTGCGCTGCGCTGCGCTT 1140
 421 TTCCCGCGCTGTGGCCGTGGCGCGCGCGCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCG 1200
 441 CGCGTCCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCG 1260
 461 AGGCTGCTGGCTGGTGGCGCGCGCGCGCGCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCG 1320
 481 GAGGCTGCCCGAGGACCGGAATAAACCTGCGCGCTGGACTCGCGCTGTGTCCGTCTGT 1380
 501 TCACCTCCCGTCTCCGAAGGCGGACGCCACCGGGCCAGGATGGGGCAATGCCACGAGC 1417
 521 TCTCTAGGGCGCTTGAAGTGGAGCGACTTGTCCCCCGC

[illegible]

FIGURE 5A

hGALR3	M A D A Q N I S L D S P G	13
rGALR3 M A D I Q N I S L D S P G	13
rGALR1	M E L A P V N L S E G N G S D P E P P A E P R P L		25
<hr/>			
hGALR3	. . . S V G A V A V P V V F A L I F L L G T V G N	I	35
rGALR3	. . . S V G A V A V P V V I F A L I F L L G M V G N		35
rGALR1	F G I G V E N F I T L V V F F A M G V L G N		50
<hr/>			
hGALR3	G L V L A V L L Q P G P S A W Q E P G S T T D L F		60
rGALR3	G L V L A V L L Q P G P S A W Q E P S S T T D L F		60
rGALR1	S L V I T V L A R S K P G . . . K P R S T T N L F		72
<hr/>			
II			
hGALR3	I L N L A V A D L C F I L C C V P F Q A T I Y T L		85
rGALR3	I L N L A V A D L C F I L C C V P F Q A T I Y T L		85
rGALR1	I L N L S I A D L A Y L L F C I P F Q A T V Y A L		97

FIGURE 5B

hGALR3 rGALR3 rGALR1	D A W L F G A L V C K A V H L L I Y L T M Y A S S	110
	D A W L F G A F V C K K T V H L L I Y L T M Y A S S	110
	P T W V L G A F I C K F I H Y F F T V S M L V S I	122
III		
hGALR3 rGALR3 rGALR1	F T L A A V S V D R Y L A V R R H P L R S R A L R T	135
	F T L A A V S L D R Y L A V R R H P L R S R A L R T	135
	F T L A A M S V D R Y V A I V H S R R S S L R V	147
IV		
hGALR3 rGALR3 rGALR1	P R N A R A A V G L V W L L A A L F S A P Y L S Y	160
	P R N A R A A V G L V W L L A A L F S A P Y L S Y	160
	S R N A L L G V G F I W A L S I A M A S P . V A Y	171
hGALR3 rGALR3 rGALR1	Y G T V . . R Y G A L E L C V P A W . E D A R R R	182
	Y G T V . . R Y G A L E L C V P A W . E D A R R R	182
	Y Q R L F H R D S N Q T F C W E H W P N Q L H K	196

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FIGURE 5C

hGALR3	A	L	D	V	A	T	F	A	A	G	Y	L	L	P	V	A	V	V	S	L	A	Y	G	R	T	207
rGALR3	A	L	D	V	A	T	F	A	A	G	Y	L	L	P	V	A	V	V	S	L	A	Y	G	R	T	207
rGALR1	A	Y	V	V	C	T	F	V	F	G	Y	L	L	P	L	L	I	C	F	C	Y	A	K	V	221	
hGALR3	L	R	F	L	W	A	A	V	G	P	A	G	A	A	A	A	E	A	R	R	R	A	T	G	R	232
rGALR3	L	C	F	L	W	A	A	V	G	P	A	G	A	A	A	A	E	A	R	R	R	A	T	G	R	232
rGALR1	L	N	H	L	H	K	K	L	K	N	M	S	K	K	S	E	A	S	K	K	.	.	.	K	242	
hGALR3	A	G	R	A	M	L	A	V	A	A	L	Y	A	L	C	W	G	P	H	H	A	L	I	L	C	257
rGALR3	A	G	R	A	M	L	A	V	A	A	L	Y	A	L	C	W	G	P	H	H	A	L	I	L	C	257
rGALR1	T	A	Q	T	V	L	V	V	V	V	V	F	G	I	S	W	L	P	H	H	V	I	H	L	W	267
hGALR3	F	W	Y	G	R	F	A	F	S	P	A	T	Y	A	C	R	L	A	S	H	C	L	A	Y	A	282
rGALR3	F	W	Y	G	R	F	A	F	S	P	A	T	Y	A	C	R	L	A	S	H	C	L	A	Y	A	282
rGALR1	A	E	F	G	A	F	P	L	T	P	A	S	F	F	F	R	I	T	A	H	C	L	A	Y	S	292

FIGURE 5D

hGALR3	N	S	C	L	N	P	L	V	Y	A	L	A	S	R	H	F	R	A	R	F	R	R	L	W	P	307
rGALR3	N	S	C	L	N	P	L	V	Y	S	L	A	S	R	H	F	R	A	R	F	R	R	L	W	P	307
rGALR1	N	S	S	V	N	P	I	I	Y	A	F	L	S	E	N	F	R	K	A	Y	K	Q	V	F	K	317
hGALR3	C	G	R	R	R	.	.	.	R	H	R	A	R	R	A	L	R	R	V	R	P	A	S	S	G	329
rGALR3	C	G	R	R	R	H	R	H	H	R	A	H	R	A	L	R	R	V	Q	P	A	S	S	G	332	
rGALR1	C	R	V	C	N	E	S	P	H	G	D	A	K	E	K	N	R	I	D	T	P	P	S	T	N	342
hGALR3	P	P	G	C	P	G	D	A	R	P	S	G	R	L	L	A	G	G	Q	G	P	E	P	R	354	
rGALR3	P	A	G	Y	P	G	D	A	R	P	R	G	W	S	M	E	P	R	350	
rGALR1	C	T	H	V	346	
hGALR3	E	G	P	V	H	G	G	E	A	A	R	G	P	E				368		
rGALR3	G	D	A	L	R	G	G	E	T	R	L	T	L	S	P	R	G	P	Q					370		

FIG. 6A

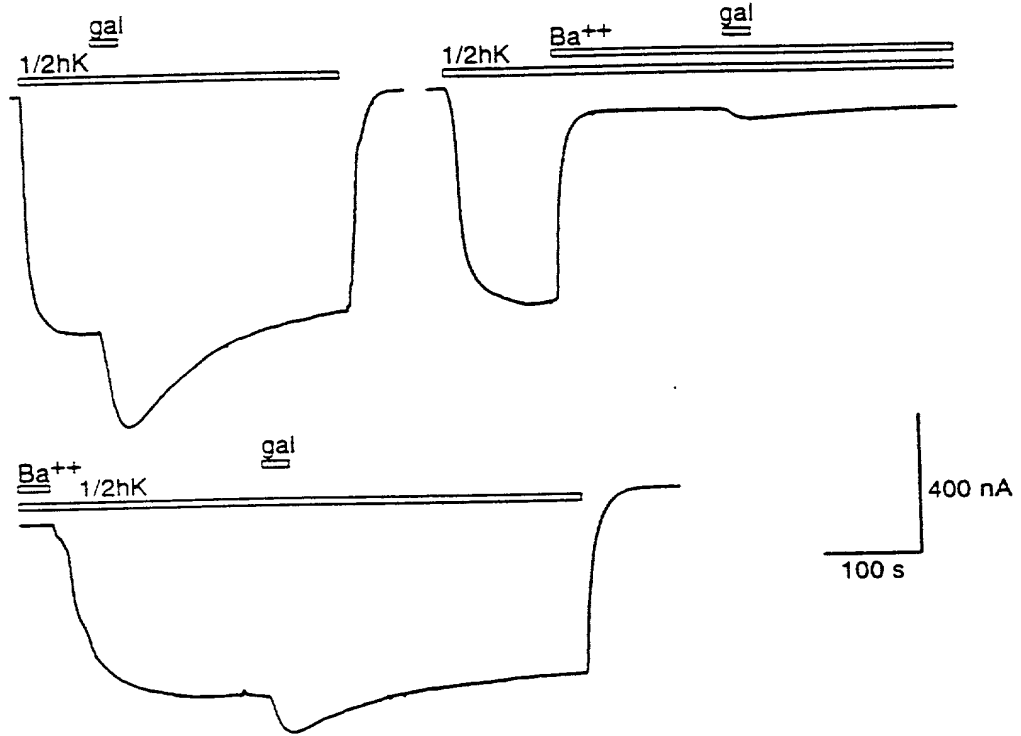


FIG. 6B

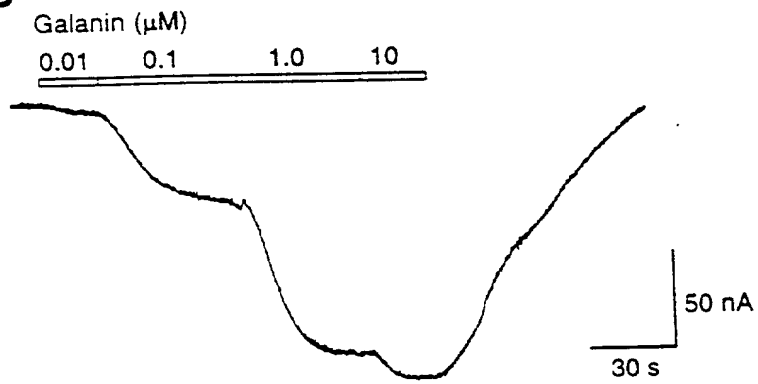


FIG. 7

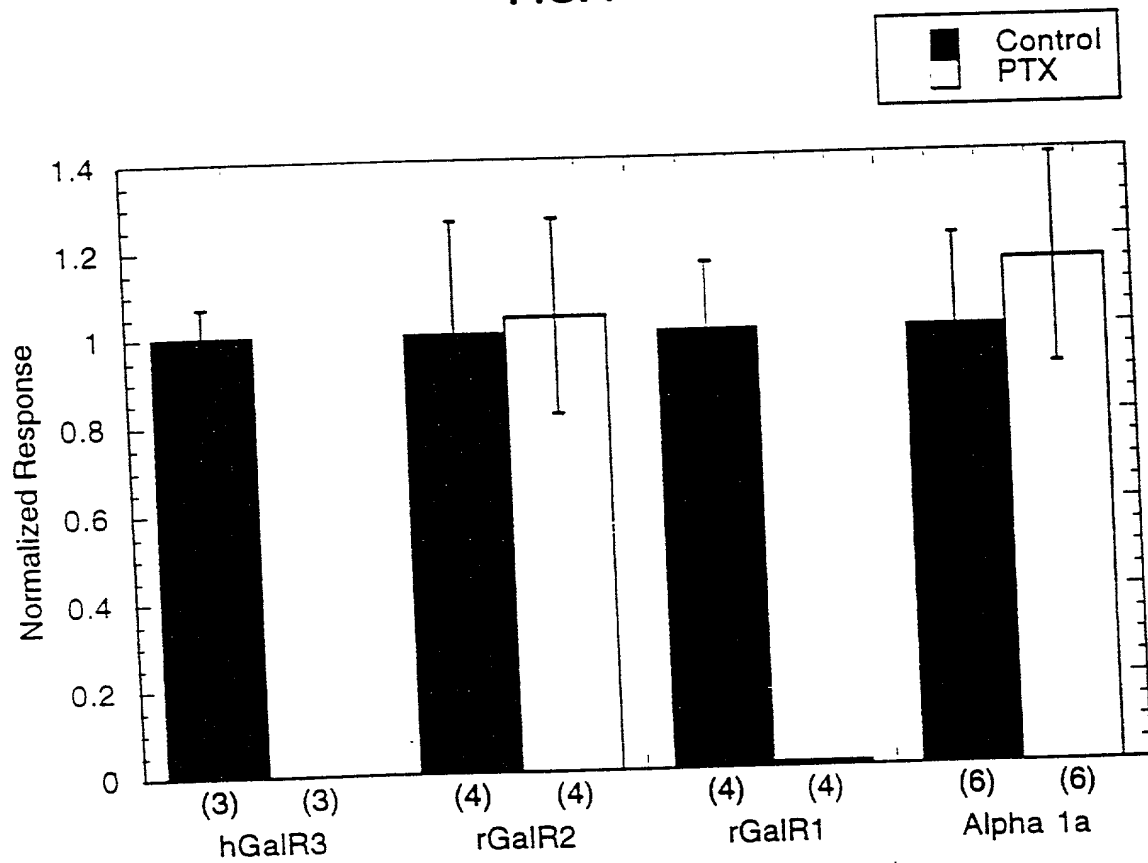


FIG. 8A

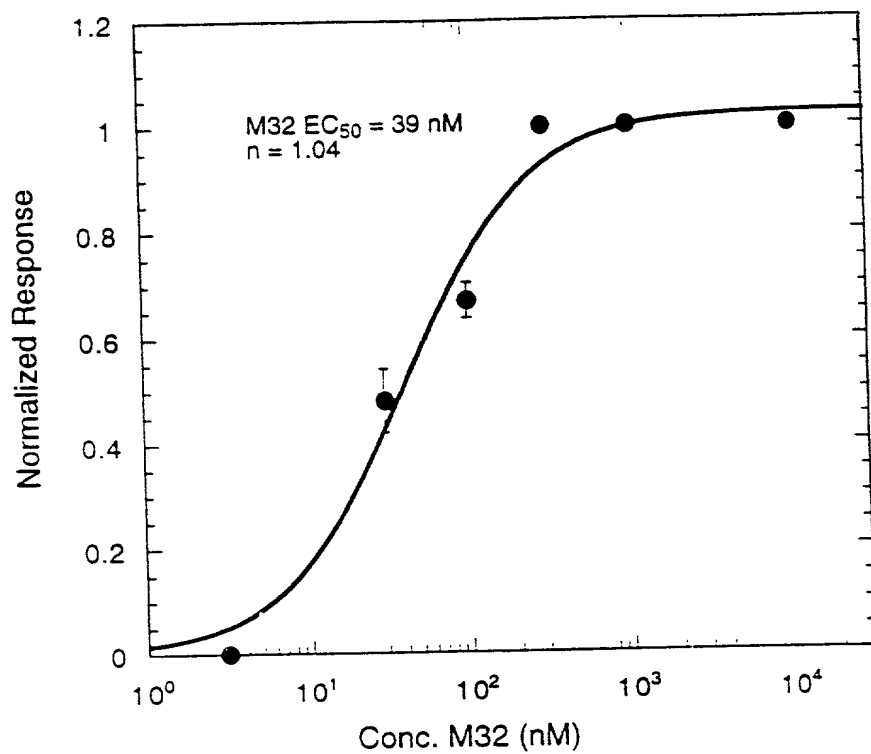


FIG. 8B

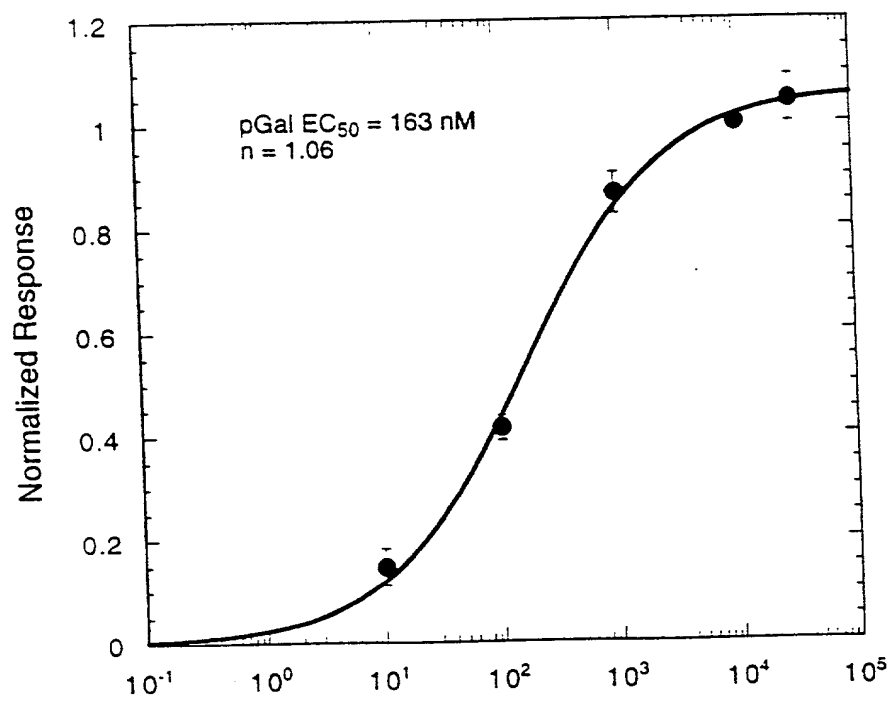


FIG. 8C

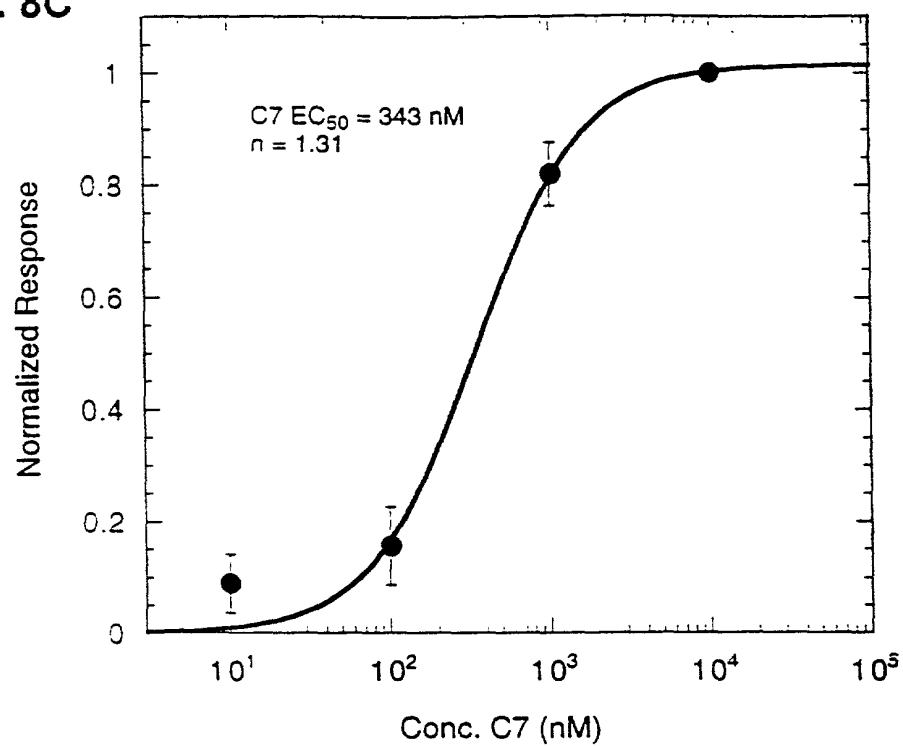


FIG. 8D

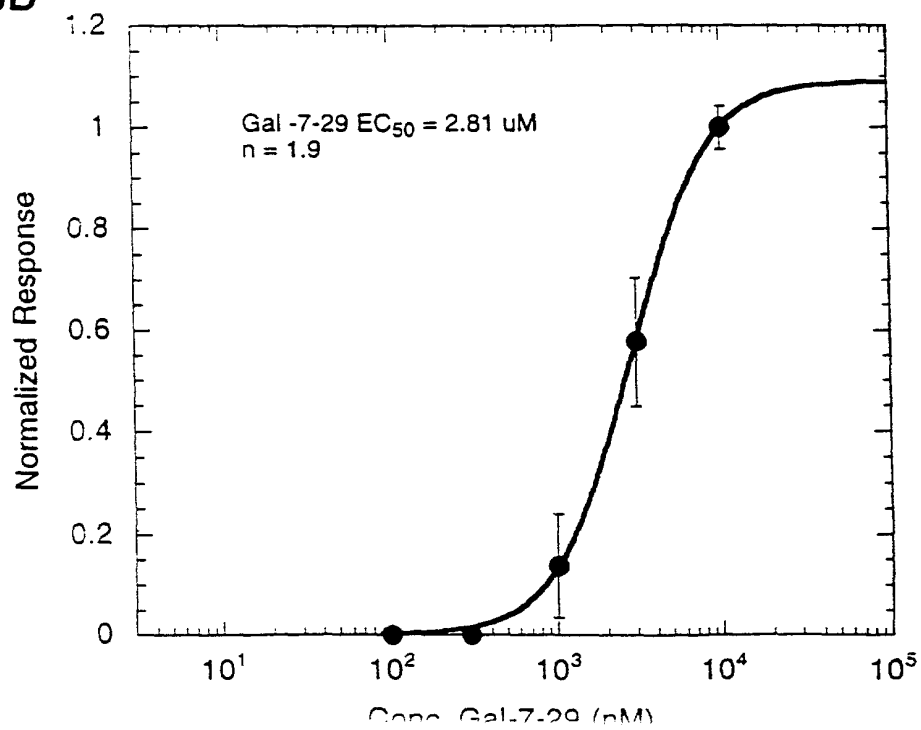


FIG. 8E

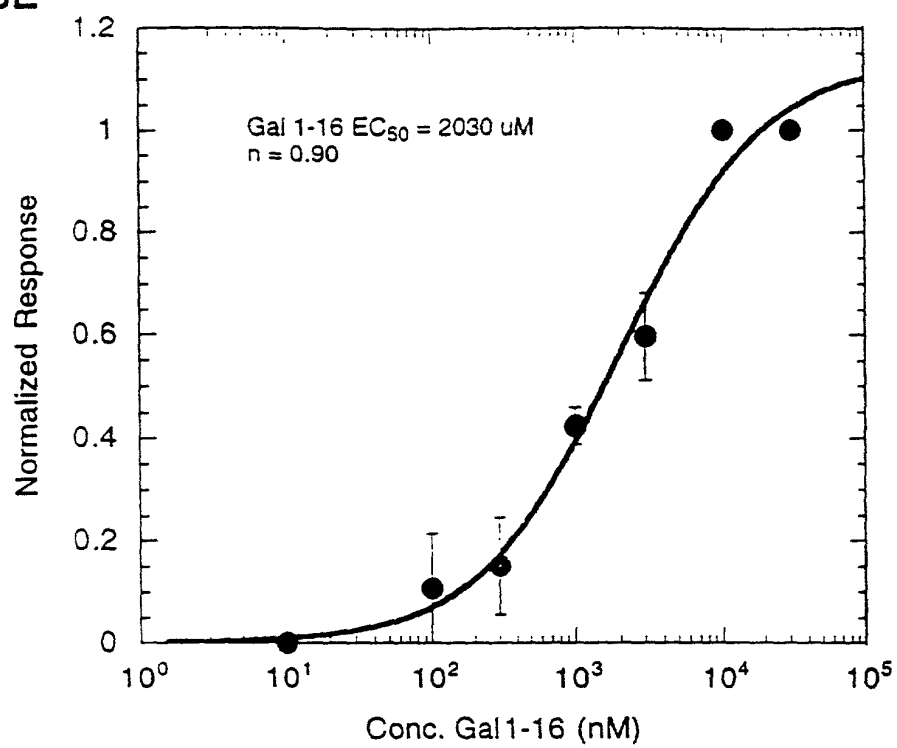


FIG. 8F

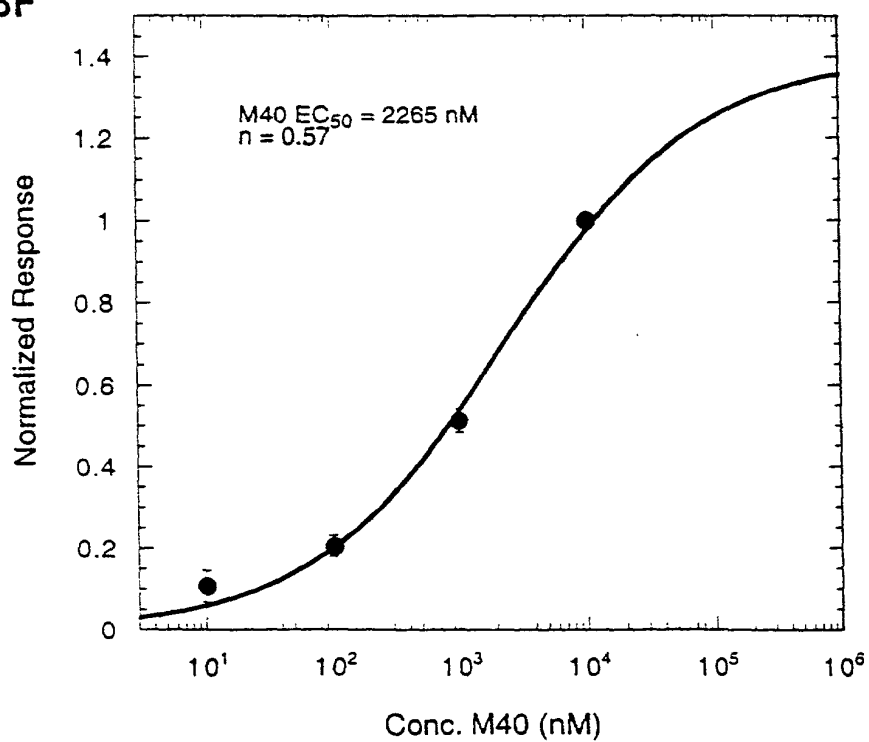


FIG. 9A

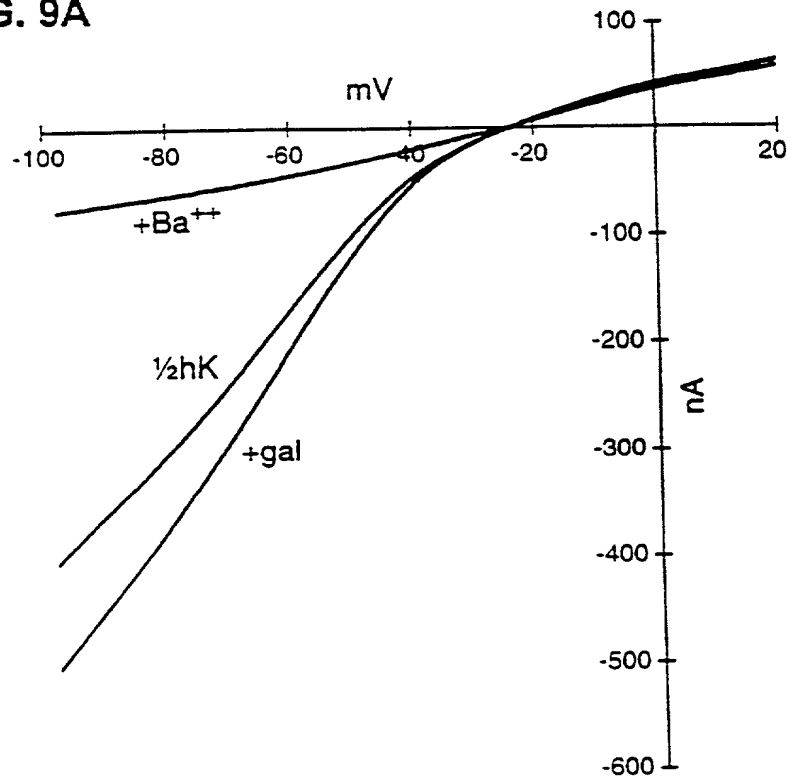


FIG. 9B

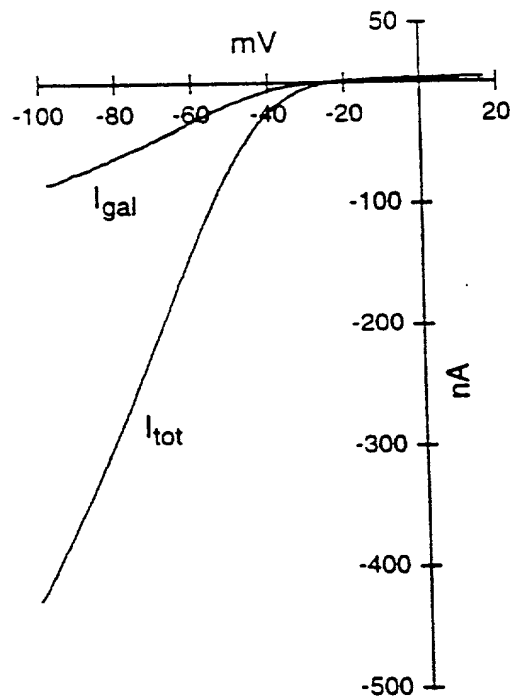


FIG. 10

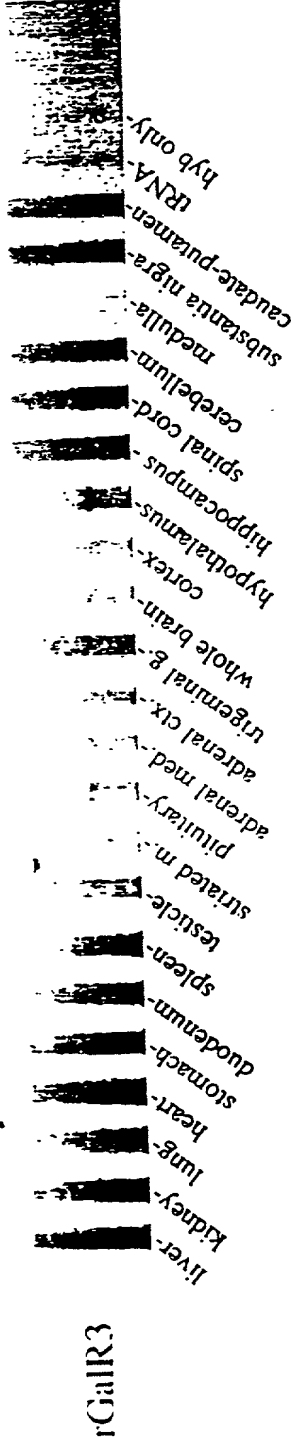


FIG. 11

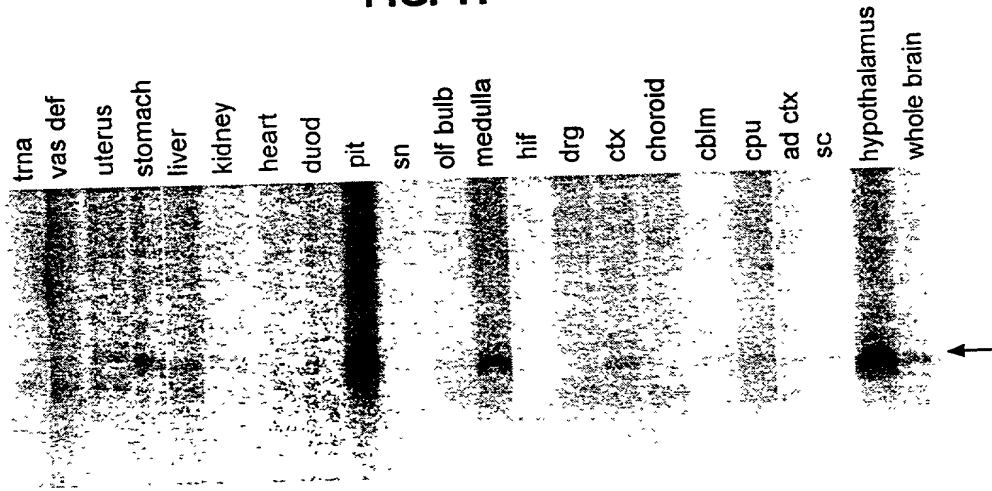


FIG. 12

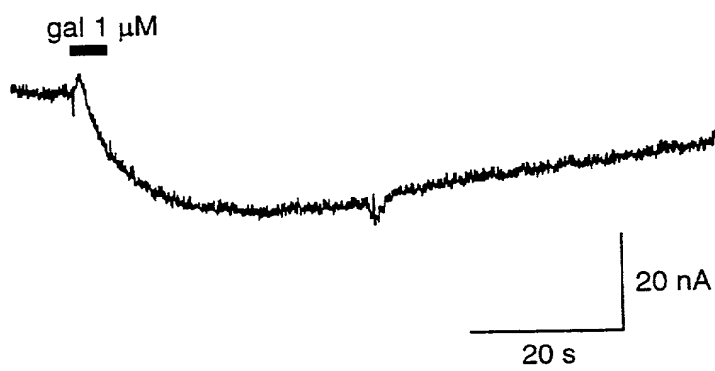


FIG. 13A
hGALR3-LM #228
+/- Pertussis Toxin

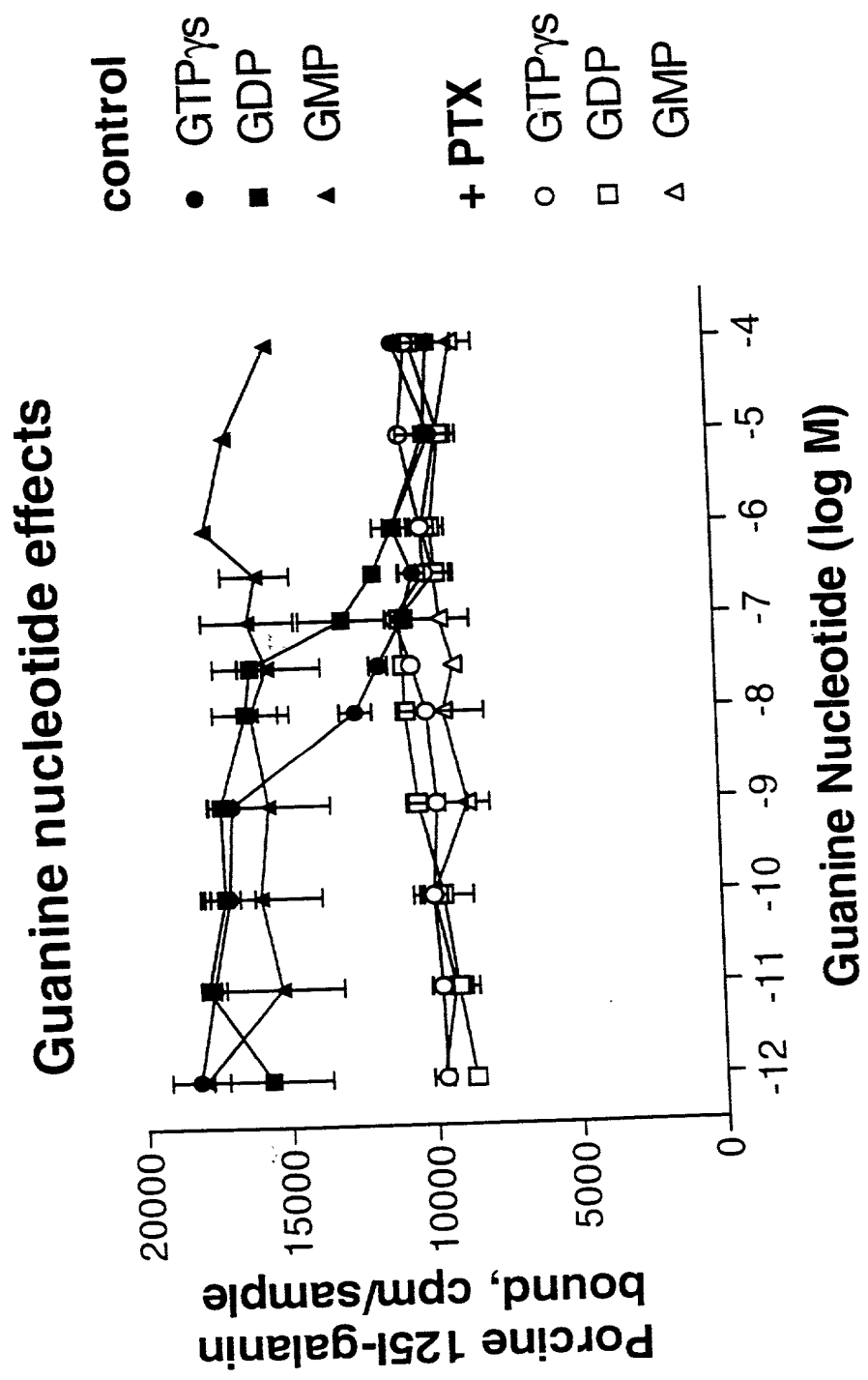


FIG. 13B
Nonspecific Binding
with 1 μ M p galanin

